Amendments to the Claims

Please amend the claims to read as follows:

1. (Currently Amended) A method of assessing relative susceptibility of a human to an undesirable bone density condition, the method comprising assessing occurrence in the human's genome of at least two known disorder-associated polymorphisms (DAPs) including:

a DAP in a gene which encodes ~~a protein that influences, by way of a transmembrane signaling pathway of a bone cell, expression of a component of bone matrix~~ vitamin D receptor; and

a DAP in a gene which encodes ~~a protein for which the level of expression of the protein is associated with bone resorption~~ interleukin-6,

whereby occurrence of any of the DAPs is an indication that the human is more susceptible to an undesirable bone density condition than a human whose genome does not comprise the DAP, and whereby occurrence of a plurality of the DAPs is an indication that the human is even more susceptible to an undesirable bone density condition than a human whose genome does not comprise the DAPs.

2-13. (Canceled)

14. (Currently Amended) The method of claim 1, wherein occurrence of an individual ~~disorder-associated polymorphism~~ DAP is assessed by

contacting a nucleic acid derived from the human's genome with a first oligonucleotide that anneals with higher stringency with the DAP than with a corresponding non-DAP and

assessing annealing of the first oligonucleotide and the nucleic acid,

whereby annealing of the first oligonucleotide and the nucleic acid is an indication that the human's genome comprises the DAP.

15. (Original) The method of claim 14, wherein the first oligonucleotide is attached to a support.

16. (Original) The method of claim 15, wherein the support has a plurality of different first oligonucleotides attached thereto.

17. (Previously Presented) The method of claim 16, wherein the support has attached thereto at least two first oligonucleotides that anneal with higher stringency with the DAPs than with the corresponding non-DAPs.

18-19. (Canceled)

20. (Original) The method of claim 14, wherein the first oligonucleotide is a molecular beacon oligonucleotide.

21. (Previously Presented) The method of claim 14, wherein occurrence of an individual DAP is further assessed by

contacting the nucleic acid with a second oligonucleotide that anneals with higher stringency with a non-DAP than with the corresponding DAP and

assessing annealing of the second oligonucleotide and the nucleic acid,

whereby annealing of the second oligonucleotide and the nucleic acid is an indication that the human's genome does not comprise the DAP.

22. (Original) The method of claim 21, wherein the second oligonucleotide is attached to a support.

23. (Original) The method of claim 22, wherein the first and second oligonucleotides are attached to the same support.

24. (Original) The method of claim 21, wherein the second oligonucleotide is a molecular beacon oligonucleotide.

25. (Original) The method of claim 24, wherein the first and second oligonucleotides are spectrally distinct molecular beacon oligonucleotides.

26. (Previously Presented) The method of claim 1, further comprising calculating a susceptibility score by summing, for each of the selected genes in which a DAP occurs in the human's genome, the product of a constant and a correlation factor, wherein the correlation factor represents the fraction of humans heterozygous or homozygous for the DAP who exhibit the corresponding disorder, whereby the susceptibility score represents the relative susceptibility of the human to an undesirable bone density condition.

27. (Original) The method of claim 26, wherein the same constant is used for each selected gene.

28-29. (Canceled)

30. (Previously Presented) The method of claim 1, wherein at least one of the DAPs is a single nucleotide polymorphism (SNP).

31. (Original) The method of claim 30, wherein occurrence of a SNP is assessed by annealing a nucleic acid derived from the human's genome with a primer that is complementary to the region adjacent the SNP on its 3' side, extending the primer using a polymerase in order to add a nucleotide residue complementary to the SNP to the primer, and detecting the identity of the nucleotide residue complementary to the SNP.

32. (Original) The method of claim 31, wherein the nucleotide residue is a non-extendable residue.

33. (Previously Presented) The method of claim 30, wherein the SNP is selected from the group consisting of

a) occurrence of a thymine residue 8 residues upstream of the normal start codon of the gene encoding vitamin D receptor, whereby the residue is part of an initiation codon and the gene encodes a variant vitamin D receptor comprising three additional amino acids at its amino terminus; and

b) occurrence of a cytosine residue at position -174 of the interleukin 6 gene promoter.

34-62. (Canceled)

63. (New) The method of claim 1, wherein the DAPs include at least:

a) occurrence of a thymine residue 8 residues upstream of the normal start codon of the gene encoding vitamin D receptor, whereby the residue is part of an initiation codon and the gene encodes a variant vitamin D receptor comprising three additional amino acids at its amino terminus; and

b) occurrence of a cytosine residue at position -174 of the interleukin 6 gene promoter.

64. (New) The method of claim 63, wherein the DAPs include at least one of:

c) occurrence of a thymine residue in the gene encoding the alpha 1 subunit of type 1 collagen at a site at which a guanine residue normally occurs, whereby a recognition site for the transcription factor Sp1 is altered;

d) occurrence of guanine residue at the position at which a cytosine residue normally occurs in the codon corresponding to amino acid residue 986 of the calcium sensing receptor gene, whereby the codon encodes a serine residue;

e) occurrence of a thymine residue at the position corresponding to position +1417 of the cDNA encoding a PtH receptor;

f) occurrence of a thymine residue at the position at which a cytosine residue normally occurs in the codon corresponding to amino acid residue 447 of the calcitonin receptor gene, whereby the codon encodes a leucine residue;

g) occurrence of a thymine residue at position +1377 of the calcitonin receptor gene; and

h) occurrence of a cytosine residue where a guanine residue normally occurs at the first nucleotide position of intron 2 of the PtH gene.